SEQUENCE LISTING

<110> MCCARTHY, JUSTIN
      CORDELL, BARBARA

<120> METHODS FOR IDENTIFYING INHIBITORS OF
   NEURONAL DEGENERATION

<130> SCIOS.012A

<160> 16

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 942
<212> DNA
<213> Homo Sapien

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aacaacaacc tcccgggcgg cgcgccggcc gcacctgccg tccccggtcc cgggggcgtg   180

aactgcgcgg tcggctccgc catgctgacg cgggcgcccc cggcccgcgg cccgcggcgg   240

tcggaggacg agccccagc cgcctctgcc tcggctgcac cgccgcccca gcgtgacgag   300

gaggagccgg acggcgtccc agagaagggc aagagctcgg gccccagtgc caggaaaggc   360

aaggggcaga tcgagaagag gaagctgcgg gagaagcggc gctccaccgg cgtggtcaac   420

atccctgccg cagagtgctt agatgagtac gaagatgatg aagcagggca gaaagagcgg   480

aaacgagaag atgcaattac acaacagaac actattcaga atgaagctgt aaacttacta   540

gatccaggca gttcctatct gctacaggag ccacctagaa cagtttcagg cagatataaa   600

agcacaacca gtgtctctga agaagatgtc tcaagtagat attctcgaac agatagaagt   660

gggttcccta gatataacag ggatgcaaat gtttcaggta ctctggtttc aagtagcaca   720

ctggaaaaga aaattgaaga tcttgaaaag gaagtagtaa cagaaagaca agaaaaccta   780

agacttgtga gactgatgca agataaagag gaaatgattg gaaaactcaa agaagaaatt

840
gatttattaa atagagacct agatgacata gaagatgaaa atgaacagct aaagcaggaa
900
aataaaactc ttttgaaagt tgtgggtcag ctgaccaggt ag
942

<210> 2
<211> 341
<212> PRT
<213> Homo Sapien

<400> 2
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Asp Trp Lys Ala Lys Arg Lys Met Arg Ala Lys Asn Gly Ala Gly Gly
            20                  25                  30
Gly Ser Ser Asp Ala Ala Gly Lys Ala Gly Ala Gly Thr Ala Ala Ala
            35                  40                  45
Ala Ala Asn Asn Asn Asn Gly Gly Ala Ala Ala Ala Val Gly Gly Gly
            50                  55                  60
Val Asn Cys Ala Val Gly Ser Ala Met Thr Arg Ala Ala Arg Gly Arg
65                  70                  75                  80
Arg Ser Asp Ala Ala Ser Ala Ser Ala Ala Arg Asp Asp Gly Val Lys
                85                  90                  95
Gly Lys Ser Ser Gly Ser Ala Arg Lys Gly Lys Gly Lys Arg Lys Arg
            100                 105                 110
Lys Arg Arg Ser Thr Gly Val Val Asn Ala Ala Cys Asp Tyr Asp Asp
            115                 120                 125
Ala Gly Lys Arg Lys Arg Asp Ala Thr Asn Thr Asn Ala Val Asn Asp
            130                 135                 140
Gly Ser Ser Tyr Arg Thr Val Ser Gly Arg Tyr Lys Ser Thr Thr Ser
145                 150                 155                 160
Val Ser Asp Val Ser Ser Arg Tyr Ser Arg Thr Asp Arg Ser Gly Arg
                165                 170                 175
Tyr Asn Arg Asp Ala Asn Val Ser Gly Thr Val Ser Ser Ser Thr Lys
                180                 185                 190
Lys Asp Lys Val Val Thr Arg Asn Arg Val Arg Met Asp Lys Met Gly
            195                 200                 205
Lys Lys Asp Asn Arg Asp Asp Asp Asp Asn Lys Asn Lys Thr Lys Val
            210                 215                 220
Val Gly Thr Arg Met Ala Thr Gly Gly Tyr Arg Thr Ser Ser Gly Gly
225                 230                 235                 240
Gly Ser Thr Thr Asp Trp Lys Ala Lys Arg Lys Met Arg Ala Lys Asn
                245                 250                 255
Gly Ala Gly Gly Gly Ser Ser Asp Ala Ala Gly Lys Ala Gly Ala Gly
            260                 265                 270
Thr Ala Ala Ala Ala Ala Asn Asn Asn Asn Gly Gly Ala Ala Ala Ala
            275                 280                 285
```

```
Val Gly Gly Gly Val Asn Cys Ala Val Gly Ser Ala Met Thr Arg Ala
    290                 295                 300
Ala Arg Gly Arg Arg Asp Ala Ala Ser Ala Ser Ala Ala Arg Asp Asp
305                     310                 315                 320
Gly Val Lys Gly Lys Ser Ser Gly Ser Ala Arg Lys Gly Lys Gly Lys
                325                 330                 335
Arg Lys Arg Lys Arg
                340
```

<210> 3
<211> 1404
<212> DNA
<213> Homo Sapien

<400> 3
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120
agacggagcc ttggccaccc tgagccatta tctaatggac gaccccaggg taactcccgg
180
caggtggtgg agcaagatga ggaagaagat gaggagctga cattgaaata tggcgccaag
240
catgtgatca tgctctttgt ccctgtgact ctctgcatgg tggtggtcgt ggctaccatt
300
aagtcagtca gctttttatac ccggaaggat gggcagctaa tctataccccc attcacagaa
360
gataccgaga ctgtgggcca gagagccctg cactcaattc tgaatgctgc catcatgatc
420
agtgtcattg ttgtcatgac tatcctcctg gtggttctgt ataaatacag gtgctataag
480
gtcatccatg cctggcttat tatatcatct ctattgttgc tgttcttttt ttcattcatt
540
tacttggggg aagtgtttaa aacctataac gttgctgtgg actacattac tgttgcactc
600
ctgatctgga attttggtgt ggtgggaatg atttccattc actggaaagg tccacttcga
660
ctccagcagg catatctcat tatgattagt gccctcatgg ccctggtgtt tatcaagtac
720
ctccctgaat ggactgcgtg gctcatcttg ctgtgatttc agtatatga tttagtggct
780
gttttgtgtc cgaaaggtcc acttcgtatg ctggttgaaa cagctcagga gagaaatgaa
840
acgcttttc cagctctcat ttactcctca caatggtgt ggttggtgaa tatggcagaa
900
ggagacccgg aagctcaaag gagagtatcc aaaaattcca agtataatgc agaaagcaca
960
```

gaaagggagt cacaagacac tgttgcagag aatgatgatg gcgggttcag tgaggaatgg
1020

gaagcccaga gggacagtca tctagggcct catcgctcta cacctgagtc acgagctgct
1080

gtccaggaac tttccagcag tatcctcgct ggtgaagacc cagaggaaag gggagtaaaa
1140

cttggattgg gagatttcat tttctacagt gttctggttg gtaaagcctc agcaacagcc
1200

agtggagact ggaacacaac catagcctgt ttcgtagcca tattaattgg tttgtgcctt
1260

acattattac tccttgccat tttcaagaaa gcattgccag ctcttccaat ctccatcacc
1320

tttgggcttg ttttctactt tgccacagat tatcttgtac agccttttat ggaccaatta
1380

gcattccatc aattttatat ctag
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<210> 4
<211> 467
<212> PRT
<213> Homo Sapien

<400> 4

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Ser Glu Asp Asn His Leu Ser Asn Thr Val Arg Ser Gln Asn Asp Asn
            20                  25                  30
Arg Glu Arg Gln Glu His Asn Asp Arg Arg Ser Leu Gly His Pro Glu
        35                  40                  45
Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val Val Glu
    50                  55                  60
Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly Ala Lys
65                  70                  75                  80
His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val Val Val
                85                  90                  95
Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp Gly Gln
                100                 105                 110
Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly Gln Arg
            115                 120                 125
Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val Ile Val
            130                 135                 140
Val Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys Tyr Lys
145                 150                 155                 160
Val Ile His Ala Trp Leu Ile Ile Ser Ser Leu Leu Leu Leu Phe Phe
                165                 170                 175
Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn Val Ala
                180                 185                 190
Val Asp Tyr Ile Thr Val Ala Leu Leu Ile Trp Asn Phe Gly Val Val
```

```
            195                 200                 205
Gly Met Ile Ser Ile His Trp Lys Gly Pro Leu Arg Leu Gln Gln Ala
    210                 215                 220
Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile Lys Tyr
225                 230                 235                 240
Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser Val Tyr
                245                 250                 255
Asp Leu Val Ala Val Leu Cys Pro Lys Gly Pro Leu Arg Met Leu Val
                260                 265                 270
Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu Ile Tyr
                275                 280                 285
Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp Pro Glu
                290                 295                 300
Ala Gln Arg Arg Val Ser Lys Asn Ser Lys Tyr Asn Ala Glu Ser Thr
305                 310                 315                 320
Glu Arg Glu Ser Gln Asp Thr Val Ala Glu Asn Asp Asp Gly Gly Phe
                325                 330                 335
Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro His Arg
                340                 345                 350
Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Ser Ser Ile
                355                 360                 365
Leu Ala Gly Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly Leu Gly
                370                 375                 380
Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala Thr Ala
385                 390                 395                 400
Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile Leu Ile
                405                 410                 415
Gly Leu Cys Leu Thr Leu Leu Leu Leu Ala Ile Phe Lys Lys Ala Leu
                420                 425                 430
Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr Phe Ala
                435                 440                 445
Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe His Gln
                450                 455                 460
Phe Tyr Ile
465


<210> 5
<211> 1346
<212> DNA
<213> Homo Sapien

<400> 5
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atgtcggccg agagccccac gccgcgctcc tgccaggagg gcaggcaggg cccagaggat
120
ggagagaaca ctgcccagtg gagaagccag gagaacgagg aggacggtga ggaggaccct
```

180
gaccgctatg tctgtagtgg ggttcccggg cggccgccag gcctggagga agagctgacc
240
ctcaaatacg gagcgaagca cgtgatcatg ctgtttgtgc ctgtcactct gtgcatgatc
300
gtggtggtag ccaccatcaa gtctgtgcgc ttctacacag agaagaatgg acagctcatc
360
tacacgacat tcactgagga cacaccctcg gtgggccagc gcctcctcaa ctccgtgctg
420
aacaccctca tcatgatcag cgtcatcgtg gttatgacca tcttcttggt ggtgctctac
480
aagtaccgct gctacaagtt catccatggc tggttgatca tgtcttcact gatgctgctg
540
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720
ctagtgttca tcaagtacct cccagagtgg tccgcgtggg tcatcctggg cgccatctct
780
gtgtatgatc tcgtggctgt gctgtgtccc aaagggcctc tgagaatgct ggtagaaact
840
gcccaggaga gaaatgagcc catattccct gccctgatat actcatctgc catggtgtgg
900
acggttggca tggcgaagct ggaccctcc tctcagggtg ccctccagct ccctacgac
960
ccggagatgg aagaagactc ctatgacagt tttggggagc cttcatacc cgaagtcttt
1020
gagcctccct tgactggcta cccaggggag ggctggagga agaggaggaa aggggcgtga
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1260
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1346

<210> 6
<211> 448
<212> PRT
<213> Homo Sapien

<400> 6

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Arg Thr Ser Leu Met Ser Ala Glu Ser Pro Thr Pro Arg Ser Cys Gln
             20                  25                  30
Glu Gly Arg Gln Gly Pro Glu Asp Gly Glu Asn Thr Ala Gln Trp Arg
         35                  40                  45
Ser Gln Glu Asn Glu Glu Asp Gly Glu Glu Asp Pro Asp Arg Tyr Val
     50                  55                  60
Cys Ser Gly Val Pro Gly Arg Pro Pro Gly Leu Glu Glu Glu Leu Thr
65                  70                  75                      80
Leu Lys Tyr Gly Ala Lys His Val Ile Met Leu Phe Val Pro Val Thr
                 85                  90                  95
Leu Cys Met Ile Val Val Val Ala Thr Ile Lys Ser Val Arg Phe Tyr
                100                 105                 110
Thr Glu Lys Asn Gly Gln Leu Ile Tyr Thr Thr Phe Thr Glu Asp Thr
             115                 120                 125
Pro Ser Val Gly Gln Arg Leu Leu Asn Ser Val Leu Asn Thr Leu Ile
     130                 135                 140
Met Ile Ser Val Ile Val Val Met Thr Ile Phe Leu Val Val Leu Tyr
145                 150                 155                 160
Lys Tyr Arg Cys Tyr Lys Phe Ile His Gly Trp Leu Ile Met Ser Ser
                165                 170                 175
Leu Met Leu Leu Phe Leu Phe Thr Tyr Ile Tyr Leu Gly Glu Val Leu
             180                 185                 190
Lys Thr Tyr Asn Val Ala Met Asp Tyr Pro Thr Leu Leu Leu Thr Val
             195                 200                 205
Trp Asn Phe Gly Ala Val Gly Met Val Cys Ile His Trp Lys Gly Pro
     210                 215                 220
Leu Val Leu Gln Gln Ala Tyr Leu Ile Met Ile Ser Ala Leu Met Ala
225                 230                 235                 240
Leu Val Phe Ile Lys Tyr Leu Pro Glu Trp Ser Ala Trp Val Ile Leu
                245                 250                 255
Gly Ala Ile Ser Val Tyr Asp Leu Val Ala Val Leu Cys Pro Lys Gly
                260                 265                 270
Pro Leu Arg Met Leu Val Glu Thr Ala Gln Glu Arg Asn Glu Pro Ile
         275                 280                 285
Phe Pro Ala Leu Ile Tyr Ser Ser Ala Met Val Trp Thr Val Gly Met
     290                 295                 300
Ala Lys Leu Asp Pro Ser Ser Gln Gly Ala Leu Gln Leu Pro Tyr Asp
305                 310                 315                 320
Pro Glu Met Glu Glu Asp Ser Tyr Asp Ser Phe Gly Glu Pro Ser Tyr
                325                 330                 335
Pro Glu Val Phe Glu Pro Pro Leu Thr Gly Tyr Pro Gly Glu Glu Leu
             340                 345                 350
Glu Glu Glu Glu Glu Arg Gly Val Lys Leu Gly Leu Gly Asp Phe Ile
         355                 360                 365
Phe Tyr Ser Val Leu Val Gly Lys Ala Ala Ala Thr Gly Ser Gly Asp
     370                 375                 380
```

```
Trp Asn Thr Thr Leu Ala Cys Phe Val Ala Ile Leu Ile Gly Leu Cys
385                 390                 395                 400
Leu Thr Leu Leu Leu Leu Ala Val Phe Lys Lys Ala Leu Pro Ala Leu
                405                 410                 415
Pro Ile Ser Ile Thr Phe Gly Leu Ile Phe Tyr Phe Ser Thr Asp Asn
                420                 425                 430
Leu Val Arg Pro Phe Met Asp Thr Leu Ala Ser His Gln Leu Tyr Ile
            435                 440                 445
```


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<210> 7
<211> 371
<212> DNA
<213> Homo Sapien
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120
tttgccgcgg cactttccgc gcggcggaag agcgcgcgcc agcttcggca cacctgggag
180
ccggatccca gccctacgcc tcgtcccgta caagctcctc caagccccgc cggctgctgt
240
gggagcggcg gccgtccctc tcctggaggt cgtctcctgg catcctcggg gccgcaggaa
300
ggaagaggag gcagcggccg gagccctggt gggcggcctg aggtgagagc ccgaccggcc
360
cctttgggaa t
371
```

```
<210> 8
<211> 5935
<212> DNA
<213> Homo Sapien
```

```
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<221> CDS
<222> (5832)...(5935)
```

```
<221> intron
<222> (5214)...(5690)
```

```
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ggccaggcac ggtggctcac gcctctaatc ccagcatttt gggaggctga ggcaggtgga
120
```

```
tcatgaggtc aggagttcaa gaccaacctg accaacatgg tgaagccccg tctctactaa
180
aaatacaaaa attaaccagg cgtgtgtgcc tgtaatccca gctactcagg aggctgaggc
240
aggagaatcg cttgaacccg aaaggtgaag gttgctgtga gcctagatca ggccactgca
300
ctctgacctg ggcgacagag cgagactcca tgtcaaagaa aaagaaagag gataagaaaa
360
tttcctaact ggaaggcaga tagctgatta aaagggtcca ctgactgcat aacataataa
420
tgataaaaga ccaaatcaga gcatatcttc aagatatttc agaggatcta agtaagaaga
480
tccaaaaatt ttgagacaga aaatacaatg caatcagaat gccactggtc ttctaaacag
540
caactctgga aactagatga taataaagca atgccttcaa aattatgaag gaaaatgctt
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660
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720
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780
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840
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1380
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1440
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1500
tatgaaaagt atatgtgtgg ccgggcatgg tggctcatgc ctgtaatccc agaactttgg
1560
```

```
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1620
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1680
cgtggtggca gccacctgta gtcccagcta ctcaggaggc tgaggcagga gaatggcgtg
1740
aacccgggag gcggagcttg cagtgagccg agatcgcgcc actgcactcc agcctgggag
1800
acagagcgag actccatctc aaaaaaaaag aaaaaaaaaa gaaaagaaa agaaaagtat
1860
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1920
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1980
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2040
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2100
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2160
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2220
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2280
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2340
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2460
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2520
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2580
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2640
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2700
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2760
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2820
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2880
tattatcccc attttatatg taagtaaaca gaggcacaaa agttaagcaa cttgcccaaa
2940
gccacacaag tcagtagcag ccaaaattcc tgactcagaa cctattaaca ctaagagaac
3000
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3060
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3120
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3180
ccttcctcga atcaagcaca ttttatgtgc agtgtcagtt cttaagacag cttaaatata
3240
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3360
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3420
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3480
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3540
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3720
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3960
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4080
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4140
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4200
gagaggcaga gacagggtta aggggaaaac tccaagactg gaatcgccaa tacaataaac
4260
tgtcgaactg agttttttct cccgcaaccc taagatacta gtaagtcctt cctcttagcc
4320
aacccttttc accagggcac cgcagttttc ttagaaggag ggtgctgggt ttgtctcagg
4380
tctttctatt ctcctgcccg ctgccctagt acatctgaaa agggagcagc gactaggaaa
4440
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agagacacgt gggtattttc ccatcctgtc tagtcattcc ctgaatcatc acaagttatc
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